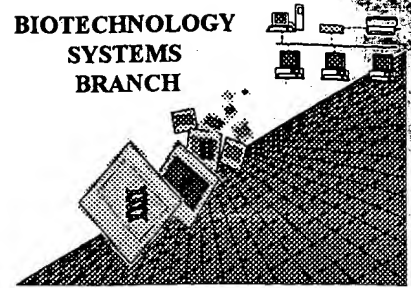


J. Burke

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/940,544A
Art Unit / Team No. : 1642
Date Processed by STIC: 6/22/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/940,544A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

J. Burke

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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/940,544A

DATE: 06/22/1999
TIME: 16:28:59

Input Set: H940544A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

E--> 1 <110> *See item B on Eva summary sheet*
E--> 2 <120> *for replacement of missing mandatory items*
W--> 3 <130>
4 <140> US/08/940,544A
5 <141> 1997-09-30
6 <160> 4
7 <170> PatentIn Ver. 2.0
8 <210> 1
9 <211> 27
10 <212> DNA
11 <213> HUMAN
12 <220>
13 <223> Upstream primer for PCR amplification.
14 <400> 1
15 gcggccgcaa ttgaagttat gtatcct 27
16 <210> 2
17 <211> 30
18 <212> DNA
19 <213> HUMAN
20 <220>
21 <223> Downstream primer for PCR amplification.
22 <400> 2
23 tcgaggatct tgtcaggagc gataggctgc 30
24 <210> 3
25 <211> 717
26 <212> DNA
27 <213> HUMAN
28 <220>
29 <223> 5F11-scFv
30 <220>
31 <221> unsure
32 <222> (37)
33 <220>
34 <221> unsure
35 <222> (79)
36 <400> 3
W--> 37 caggtgaaac tgcagcagtc aggacctgaa ctggtgnagc ctggggcttc agtgaagata 60
W--> 38 tcttgcaaga cttctgga na caaattcact gaatacacca tgcactgggt gaagcagagc 120
39 catggaaaga gccttgagtg gattggaggt attaataccta acaatggtgg tactaactac 180
40 aagcagaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240
41 atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagagatact 300
42 acgggtcccgt ttgcttactg ggtccaaggg accacgggtca ccgtctctctc aggtggaggc 360

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/940,544A

DATE: 06/22/1999
 TIME: 16:28:59

Input Set: H940544A.RAW

```

43      gggttcaggcg gaggtggctc tggcgggtggc ggatcggaca tcgagctcac tcagtctcca 420
44      gcaatcatgt ctgcatctcc aggggagaag gtcacatga cctgcagtgg cagctcaagt 480
45      ataagttaca tgcactggta ccagcagaag cctgtcacct ccccaaaaag atggatttat 540
46      gacacatcca aactggcttc tggagtcctt gctcgttca gtggcagtgg gtctgggacc 600
47      tcttattctc tcacaatcag cagcatggag gctgtagatg ctgccactta ttactgccat 660
48      cagcggagta gttaccgct cacgttcggt gctgggacac agttggaaat aaaacgg 717
49      <210> 4
50      <211> 714
51      <212> DNA
52      <213> HUMAN
53      <220>
54      <223> 3G6-scFv
55      <400> 4
56      agtattgtga tgaccagac tcccaaattc ctgcttgtat cagcaggaga cagggttacc 60
57      ataacctgca aggccagtca gagtgtgagt aatgatgtgg cttggtacca acagaagcca 120
58      gggcagtctc cgaaactgct gatatactct gcatccaatc gctacactgg agtccctgat 180
59      cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240
60      gaagacctgg cagtttattt ctgtcagcag gattatagct cgctcggagg ggggaccaag 300
61      ctggaaataa aaggtggagg cggttcaggc ggaggtggct ctggcgggtg cggatcgag 360
62      gtgcaggtga aggagtcagg acctggcctg gtggcgccct cacagagcct gtccatcact 420
63      tgcactgtct ctgggttttc attaaccaat tatggtgtac actgggttcg ccagcctcca 480
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66      atgaacagtc tgcaaaactga tgacacagcc atgtactact gtgccagtcg ggggggtaac 660
67      tacggctatg ctttggacta ctgggggtcaa ggaacctcag tcaccgtctc ctca 714
  
```

VERIFICATION SUMMARY
PATENT APPLICATION US/08/940,544ADATE: 06/22/1999
TIME: 16:28:59

Input Set: H940544A.RAW

Line	? Error/Warning	Original Text
1	E Response to "Applicant" Name is Missing	
2	E Response to "Title of Invention" Missing	
3	W Response to "File Reference" is Missing	
37	W "N" or "Xaa" used: Feature required	caggtgaaac tgcagcagtc aggacctgaa ctggtgna
38	W "N" or "Xaa" used: Feature required	tcctgcaaga cttctggana caaattcact gaatacac